

Db	301	FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAHVFEYRGFVANTLADDAEMLRPSBT	360	QY	420	YSTLEDFSLLEGPGODKVMSEVYLGKQICNVACDGPDRVERHETLSQWNRFSGAGFAA	479
QY	360	ESVAVNSVPELHKLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPFLDRFTESHY	419	Db	473	YSTLEDFSLLEGPGODKVMSEVYLGKQICNVACDGPDRVERHETLSQWNRFSGAGFAA	532
Db	361	ESVAVNSVPELHKLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPFLDRFTESHY	420	QY	480	AHGSNAFKQASMLLAFENGEGYRVEESDGCMLGWHTRPLIATSAWKLST	531
QY	420	YSTLEDFSLLEGPGODKVMSEVYLGKQICNVACDGPDRVERHETLSQWNRFSGAGFAA	479	Db	533	AHGSNAFKQASMLLFSNFNSQGYRVEESNGLMGLGWHTRPLIATSAWKLST	584
Db	421	YSTLEDFSLLEGPGODKVMSEVYLGKQICNVACDGPDRVERHETLSQWNRFSGAGFAA	480	RESULT	3		
QY	480	AHGSNAFKQASMLLAFENGEGYRVEESDGCMLGWHTRPLIATSAWKLST	532	G96688		hypothetical protein T27F4.10 [imported] - Arabidopsis thaliana	
Db	481	AHGSNAFKQASMLLAFENGEGYRVEESDGCMLGWHTRPLIATSAWKLST	533	C;Species: Arabidopsis thaliana (mouse-ear cress)		C;Species: Arabidopsis thaliana (mouse-ear cress)	
RESULT	2	hypothetical protein At2901570 [imported] - Arabidopsis thaliana		C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001		C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	
Db	48426	hypothetical protein At2901570 [imported] - Arabidopsis thaliana		C;Accession: G96688		C;Accession: G96688	
C;Accession: D84426		C;Accession: D84426		R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maiti, R.; Khaykin, E.; Kim, R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Umayam, L.; Talion, L.; Euss, D.; Neiman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature, 402, 761-768, 1999		R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maiti, R.; Khaykin, E.; Kim, R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Umayam, L.; Talion, L.; Euss, D.; Neiman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature, 402, 761-768, 1999	
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.		A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.		A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.		A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	
A;Reference number: A84420; MUID: 20083487		A;Reference number: A84420; MUID: 20083487		A;Accession: G96688		A;Accession: G96688	
A;Accession: D84426		A;Accession: D84426		A;Status: preliminary		A;Status: preliminary	
A;Status: preliminary		A;Status: preliminary		A;Molecule type: DNA		A;Molecule type: DNA	
A;Molecule type: DNA		A;Molecule type: DNA		A;Residues: 1-511 <STO>		A;Residues: 1-511 <STO>	
A;Cross-references: GB:AE002093; PIDN:93785986; NID:93785986; PIDN: AAC67333.1; GSPDB:GN00139		A;Cross-references: GB:AE002093; PIDN:93785986; NID:93785986; PIDN: AAC67333.1; GSPDB:GN00139		C;Genetics:		C;Genetics:	
C;Genetics:		C;Genetics:		A;Gene: T27F4.10		A;Gene: T27F4.10	
A;Map position: 2		A;Map position: 2		A;Map position: 1		A;Map position: 1	
Query Match	79.2%	Score 2185.5; DB 2; Length 587;		Query Match	57.5%	Score 1587; DB 2; Length 511;	
Best Local Similarity	74.3%	Pred. No. 6.8e-155; Mismatches 39; Indels 44; Gaps 9;		Best Local Similarity	59.0%	Pred. No. 2.2e-110; Mismatches 74; Indels 44; Gaps 9;	
Matches	440;	Conservative		Matches	319;	Conservative	
QY	1	MKRDHHHH--HH-----QDKRMMNNEDDGNGM-----DELLAVLGKVKRSSEMA 43		QY	1	MKRDHHHHHOD-----KTKTMMNEEDDNGMDELLAVLGKVKRSSEMAQKLEQLEV 55	
Db	1	MKRDHHQFOGRLSNHGTSSSSSTSLSKDKMMVKEEDGGNMMDDELLAVLGKVKRSSEMA 60		Db	1	MKREHNRRESSAGEGGSSSSMTTV1KEEAGSYDVEDELLVGTVKRSSEMAQKLEQLEV 60	
QY	44	DVAQKLEQEVIMMSNQEDDLISOLATEVHYPAELYTWLDSMLTDLNPP----SSN-- 96		Qy	56	MSNVQDIDISQOLATEVHYPAELYTWLDSMLTDLNPP-----PSSNAYDIAKEDPLINP 111	
Db	61	EVALKLEQEVIMMSNQEDGLSHLTDVHYNPSLYSMLDNLSEUNPPPASSNGLD 120		Db	61	LG-----DGISNLSDETVHNPDSLGSWMSLSDLPTRIQEKPDSEYDLRATIPSAYV 116	
QY	97	-----AEYDLKAPGDAILNQFAIDSASSSNQGGGDTYTNNKLK-CSV----- 140		Qy	112	QFALDSASSSNQGGGDTYT-----NKRKCNSNGVYETTATAESTRHYVLYDQSENGVRLV 169	
Db	121	PVLPSPEICGFPDYDLKVPGNAYIQFPADSSSSN-----QNKRKLKSCSSPD 172		Db	117	R-----DEHTTRRSRTRTSEL-----SSPSVSVVLDQSQETGVRLV 153	
QY	141	-----GVV-----ETTATAESTRHVLYDQSENGVRLHALLACABV 179		Qy	170	HALLACAEAVOKENLTVAELAVKQIGFLAVSQIGAMRKVATYFAELARRYRLSPQSP 229	
Db	173	SMVTSSTGTQIGVGTVTTTTAAGESTRSVLVDQSENGVRLHALLACABV 232		Db	154	HALLACAEAVQNNLKLADALVKHIVGLASSQAGAMRKVATYFAELARRYRLSPRDDV 213	
QY	180	QKENLTVAELVKQIGFLAVSQIGAMRKVATYFAELARRYRLSPSOPIDHSLSDTQ 239		Qy	230	IDHLSLSDTQLMHETCPLKFAHTANQALEAFQKRVHIDFSMSQGLOMPALQALALRPGGPPV 289	
Db	233	QNNLTLTAAELVKQIGFLAVSQIGAMRKVATYFAELARRYRLSPSOPONOIDCLSDTQ 292		Db	214	ALSSFSDTLQIHEYFESCPYKLFKAHTANQALEFATAEVHVIDGLNLNGLQWPALIQA 273	
QY	240	MHFYETCPYKLFKAHTANQALEAFQKRVHIDFSMSQGLOMPALQALALRPGGPPV 299		Qy	290	LALRPGGPPVERLTGIGPAPDNFDYLHEVGCKLAHLAEAHVFEYRGFVANTLADLDA 349	
Db	293	MHFYETCPYKLFKAHTANQALEAFQKRVHIDFSMSQGLOMPALQALALRPGGPPV 352		Db	274	LALRPGGPPVERLTGIGPAPDNFDYLHEVGCKLAHLAEAHVFEYRGFVANTLADLDA 329	
QY	300	FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAHVFEYRGFVANTLADDAEMLRPSBT 359		Qy	350	SMLELRPSELESVAVNSFEELKLLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPIF 409	
Db	353	FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAHVFEYRGFVANTLADDAEMLRPSBT 412		Db	330	EMLD1RPG-LESVAVNSFEELKLLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPIF 388	
Qy	360	ESVAVNSVPELHKLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPFLDRFTESHY 419		Qy	410	LDRFTESLHYYSTLEDSLEVPSGDKWSEVYLGKQICNVACDGPDRVERHETLQW 469	
Db	413	ESVAVNSVPELHKLGRPAIDKVLGVNNQIKPEIIFTYVEQESNHNSPFLDRFTESHY 472		Db	389	LDRFTESLHYYSSLFDSLEGPSS-QDRVMSSELFGRQILNLVACEGEDRVVERHETLNQWR 447	

RESULT 4

RGA-Like Protein - Arabidopsis thaliana
N;Alternate names: protein K1M16_60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
R;Sato, S.; Nakamura, Y.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z225394
A;Accession: T51475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <SAT>
A;Cross-references: EMBL:AL391150
C;Genetics:
A;Map position: 5
A;Note: K1M16_60

Query Match 54.0%; Score 1490; DB 2; Length 523;
Best Local Similarity 57.3%; Pred. No. 3.8e-103; Gaps 14;

Matches 315; Conservative 78; Mismatches 105; Indels 52; Gaps 14;

Db 1 MKRDHHHHQDKTMMNNE-DDGNG-----MDELLAIVGYKVRSSNEADVAQKLEOLE 53
Db 1 MKRSHQETSVEEEAPSMEVERLENGCGGGEDDNMPDFLAVGYKVRSSNDVAQKLEOLE 60

Qy 54 VMMSVNQEDL-- SQQATEVHYNPAELYTWLDSMLTDN-- -PSSSNAEYDLKAIPCD 107
Db 61 MVLSN---DIASSSNAFNDVHYNPSLDSGWAQSMSLDSNQYPDLDPRICDRLRPTID 116
Qy 108 AILNOFAIDSASSNQGGGDTYTNNKRLK-- -CSNGVVEITTTATAESTRHVLVDSQE 163
Db 117 -----DECCSSNS-----NSNKRKLRGLPNCD-----SNTSESTRSVLII-BE 152

Qy 164 NGVRLVHALLACABAVOKENLYAELVKQIGFLAVSQTIGAMRKVATYFAEALAR - 223
Db 153 TGVRLVQALVACAEBAVLENLSDALVYRVLIAASQAGMGRVATYFAEALARVYI 212

Qy 224 SPSQSPIDHSLSDFLQMHFYYETCPYKLFKAHTQANQALFAQGQKKRHYVIDFMSMSQGLW 283
Db 213 HPSAAADPSFEEITQMNNTYDSCSYLKFAHTQANQALFAQGQKKRHYVIDFMSMSQGLW 272

Qy 284 PALMOALARPQGPVFRGLGIGPAPDNFDLYHEVGKCLKLAIAEIAHVEFVYRGFVANT 343
Db 273 PALMOALARPQGPSPRLTGVNPS- NREGIOELGWKLQALQAQIGVEFKENGILTER 330

Qy 344 LADLDASMLELPSETESEVANVSFELHLGRGAIKDVLGVVNNQIKPEIIFTYVEQESN 403
Db 331 LSDLEPDMPETR-TESETLVVNSFELHVLSQFSIEKLAVKAVRGPVTVVEQEAN 389

Qy 404 HNSPIELDFRTESIHYSYPLFDSLEG-- -VPSGQDKVMSSEVYLGKQTCNVACDGPDRVE 460
Db 390 HNGDVFELDNEAHYHSSLEDFDGVVTPS- QDRVNESEVYLGQIUNLVATEGSDRVE 448

Qy 461 RHETLISQWRNRFGSAGFAAAHIGSNAFAKOASMLALFNGEGYRVEESDGLMIGWHRP 520
Db 449 RHETLAORKRMGSAGFDPVNLGSDAFQASLLLSGGDGYRVEENDGSLMLAQTKP 508

Qy 521 LIATSAWKLS 530
Db 509 LIAASAWKLA 518

RESULT 5

T47581 - Arabidopsis thaliana
N;Alternate names: protein F24B22_180
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47581
A;Reference number: Z23016
A;Submitted to the Protein Sequence Database, January 2000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-653 <BL0>
A;Cross-references: EMBL:AL132957
A;Experimental source: cultivar Columbia; BAC clone F24B22
C;Genetics:
A;Map position: 3
A;Introns: 511/2
A;Note: F24B22_180

Query Match 54.0%; Score 602.5; DB 2; Length 653;
Best Local Similarity 30.9%; Pred. No. 7e-37; Gaps 18;

Matches 173; Conservative 85; Mismatches 186; Indels 115; Gaps 18;

Qy 54 VMMSS--NVQEDDLISOLATEVHYNPAELYTWLDSMLTDLNPPSSNA----- 97
Db 121 VMMSVQPMDDQDSSSSASPV-----WDAITRDLHSSTSVPOLIQVNVRDIF 171

Qy 98 -----EYDLKAIPDAILNOFAIDSASSNN----- 122

Db 172 PCPNPNIGALLEYRLRL-----MLDOPSSSSPSPQTPELYQISNNNPSPQQQHQ 223
Qy 123 -----QGGGDTYTNNKRLKCSNGVVEITTTA-ESTRHVVLYDS 161

Db 224 QQQQOHKPPPPPIQOQERNSNSTDAPPQETVATPVQNTNAEALRERKEEIKRKQK 283
Qy 162 QENGYRLVHALLACABAVOKENLYAELVKQIGFLAVSQTIGAMRKVATYFAEALAR - 219
Db 284 DEEGLHLTLULQCA-BAVASDNLEANKLLEISOLSTPGTSQRAVAYFSEMASRLL 343

Qy 220 -----IYRLSPSQ-SPIDHSLS- -DTLQMHFYYETCPYKLFKAHTQANQALEAFGKRVH 271
Db 344 NSCLGITYAALPSRNMQPQTHSLKMYSAFQV- FNGISPLVYKFSHEFTANQAOQEAFFKEDSVH 402
Qy 272 VIDFSMSQGLQWPAIMQALARPGSPPVFRGLGIGPAPDNFDLYHEVGKCLKLAIAH 331

Db 403 IIDLDIMQGLQWPLGFHILASRPGPQPHVRLTGLG-----TSMELQATGKRLSDFADLKG 458

Qy 322 VEFYRGFVANTLADLDASMLELPSETESEVANVSFELHLGRGAIKDVLGVVNNQIK 391
Db 459 LPFEFCP-LAEKVGNLDTLNVR-KREAVAVH-WLQSLYDVTGSDAHTWLQRLIA 513

Qy 392 PEITVYQEQSNHNHSPIELDFRTESIHYSYPLFDSL-----EGVPSQDKVMSSEVYLGKQIC 448

Db 514 PKVYVTEQDGPDEVERHETLSWORNRFGSAGFAAAHIGSNAFAKOASMLALFNGEGYRVEES 508

Qy 449 NVYACDGPDEVERHETLSWORNRFGSAGFAAAHIGSNAFAKOASMLALFNGEGYRVEES 508

Db 573 NVLAVGQPSR-SGEVKFESWREKQCGPKGISLAGNAATQATLLGMF-PSDGTYLVD 630

Qy 509 DGCLMLGWHTRPLTIATSAW 527
Db 631 NGTLKLQWDLSLTSASW 649

RESULT 6

T51244 - SCARECROW protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

A; Status: preliminary								
A; Molecule type: DNA								
A; Residues: 1-482 <STO>								
A; Cross-references: GB:AE005173; NID:9454566; PIDN:AAF87889.1; GSPDB:GN00141								
C; Genetics:								
A; Gene: F11F12.22								
A; Map position: 1								
Query Match	20.5%	Score 565.5;	DB 2;	Length 482;				
Best Local Similarity	31.7%	Pred. No. 2.5e-34;						
Matches 145;	Conservative 72;	Mismatches 156;	Indels 85;	Gaps 11				
Qy	147 TATAATRHHVLLDV -SQENGVRVLLAACAEAVQENNTVAEALVKQIGFLAVSQIGA 204							
Db	31 TLLASSPPFICLKDLPKEERGLYLHLLTCANHYASGSQNANALEQLSLHSLASPDGT 90							
Qy	205 MRKVATYFAEALARRL -YRLPSQSPIDHSL-SDTQLMH -FYETCPYLKFAHFT 255							
Db	91 MORIAYAFTTEALANRNLKSPGGLYKALNAYQTRTNNVSEEHVRLRFEMEPILKVSYLL 150							
Qy	256 ANQATLEAQGKKRKHVIDSMSQGLQWPAALRPGQPPYPRLTGCPPAPDNFDY 315							
Db	151 TNRATLEAMGEKMYHVIDLDASEPAQWLTQALQFNSRSPHURITYV - - - RHQKEV 206							
Qy	316 LHEVGGKLAHAEAIVHEVFFYRGFWANTLADLASMLE-LRPSETEAVNSYFELHKLL 374							
Db	207 LEQMAHRLIEEAKEKLDPFOENPVYSR - - - LDCLNIVQEQLRVKTGEALAVSVTQLHTFL 262							
Qy	375 G-----							375
Db	263 ASDDDILMRKNCALRFQNPNPSGVDLQRVLMMMSHGSAAEARENDMSNNNNGYSPSGDSASSLPL 322							
Qy	376 -RPGAIKDVKLGVVNNQIKPKEIPTVVEQESNHNSPFLDRLFETESLHYSTLFDLSLE-GVP- 431							
Db	323 LPSSSRTDSEVNLQVQVWVYTFQDPSRHTMLLESYTYAALFDCLTKEVPR 382							
Qy	432 SGQDKRYMSE-GRQICINQVACDGPDRVERHETLQSQRNRFSGAFAAHAGNSNAFKQOA 490							
Db	383 TSQDRKIVEMFLGEEIKNNTISCGFERRERHEKLEWSORIDLAGFGNVPLSYIYMLQA 442							
Qy	491 SMLLALFNGGEGYRYVEEDGCLMLGWHTTRPLIATSAWK 528							
Db	443 RRLIQ -GCGFDGYRIKEESGGCAVICWQDRPLYSVSAWR 479							
RESULT	9							
G844662	probable SCARECROW gene regulator [imported] - <i>Arabidopsis thaliana</i>							
C; Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)								
C; Date: 02-02-2001 #text_change 02-Feb-2001								
C; Accession: GB4462								
R; Lin: X; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fu, D.; Nierman, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.								
A; Title: Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i>								
A; Reference number: A844420; MUID:20083487								
A; Accession: GB4462								
A; Status: preliminary								
A; Molecule type: DNA								
A; Residues: 1-413 <STO>								
A; Cross-references: GB:AE002093; NID:g4585920; PIDN:AAD25580.1; GSPDB:GN00139								
C; Genetics:								
A; Gene: At2904890								
A; Map position: 2								
Query Match	20.4%	Score 564;	DB 2;	Length 413;				
Best Local Similarity	34.1%	Pred. No. 2.6e-34;						
Matches 133;	Conservative 90;	Mismatches 135;	Indels 32;	Gaps 14				
Qy	156 VVLVDQSENG -VRLVHALLAACAEAVQENNTVAEALVKQI -GFLAVSQIGAMRKVATYFA 213							

Db	181	-BID-----SENSYQNESEQHQDPSKESSAD-----SNSHVSSEVVSOATPKQ	224	Db	496	SSKKT--SAADMILKAYQTYMSVCPYKKAATIFANHSMMRFTANANTIHIDFGISYGFQ	552
Qy	157	VLDSQENGVLVHALLACAAVOKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEAL	216	Qy	283	WPALMQALAI-RPGGPPVFRITGIGPPAPDNPFDLYEVGCKLAHLAEAHVFEFVYGF--	339
Db	225	ILI-----SALSECGKLEAALSMMYNEILQIVSICQDPSQRIAAIMVEGL	270	Db	553	WPALIHLRLSRSRGCGSPKLRTGJ-----	585
Qy	217	ARR-----IYR-LSPSQSPIDHSLSDTLDMHFYETCPYLKFAHFTANQAILEAFQGK	268	Qy	340	-----VANTLADDAAML-----ELRSEIESVAVNSVFEHLKLIG	375
Db	271	AARMAASGKFIYRALCKKEPESDERIA-AGQV-LFEVCPCKFGEFLAANGAILEAKGEE	328	Db	586	AAEFRROVIAWLDVTSMTMFRISTCIGL-----ELRSEIESVAVNSVFEHLKLIG	645
Qy	269	RVHVIDEFSMSQGLQWALMQALALRGGPPVFRITGIGPP-APDNEFDLYHEVGCKLAHL	326	Qy	376	RPGAI---DKVLYNQNIKPEIFTVVEQEENHNSFLDRETEIHYSTLFDSEGVGP	431
Db	329	EVHIIIDFINGQNYMTLIRLSTAELPGKPKRLRTGIDDEPSVRSIGGLRIGLRLQEL	388	Db	646	ETVLVNSPRDVALKIRKINNFTIAILSGNYNADEFVTRFREALFHSYAVFDMODSKL	705
Qy	327	AAIHEFEPYGFVANTLADASMLEPRESIEAVNSVYFELIKL--LGRCGAIDK	382	Qy	432	SGQDKV---MSEVYLGKQICNVVACDGPDRVERHETLSQWRNFGSAGFAAHIGSNAF	487
Db	389	AEDNGYSFKFKAMPSTK-SVSPSTLJCKPG--ETLIVNPAFLQHMPDBSVTTVNRD	445	Db	706	AREDERMLMYFEPY-GREIVNVNVAEGTERVESRRTYKQVQARLTRAGFQLPLEKLM	764
Qy	383	VLGVVYQNIKEPEIFTVVEQESHNQMLPDRFTESLHYSTLFDSLE-GVP-SGQDKV	439	Qy	488	KQASMLLALFNG-KGTYRVEESDGCMLGNHTRPLTATSAWKLSTN	532
Db	446	LLHMKSLNPKLTVTVEQDNTNTSEPPFIEATEYYSAVFESELDMLTUPRESQRMVNE	505	Db	765	Q--NLRKLIENGYDKNFDVONGNLLQGNGKRIYVASSLWVPSSE	808
RESULT 15							
	T51234	scarcerow-like protein 1 [imported] - Arabidopsis thaliana (fragment)					
	C;Species: Arabidopsis thaliana (mouse-ear cress)						
	C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000						
	C;Accession: T51234						
	R;Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N.						
	Plant J. 18, 111-119, 1999						
	A;Title: The GRAS gene family in Arabidopsis: sequence characterization and basic exp						
	A;Reference number: 225337; MUID: 9972994						
	A;Accession: T51234						
	A;Status: preliminary; translated from GB/EMBL/DDBJ						
	A;Molecule type: mRNA						
	A;Residues: 1-322 <PYS>						
	A;Cross-references: EMBL:AF036300; PIDN: AAD24403.1						
	C;Genetics:						
	A;Gene: SC1L1						
RESULT 14							
	T51232	scarcerow-like protein 14 [imported] - Arabidopsis thaliana (fragment)					
	C;Species: Arabidopsis thaliana (mouse-ear cress)						
	C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000						
	C;Accession: T51232						
	R;Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N.						
	Plant J. 18, 111-119, 1999						
	A;Title: The GRAS gene family in Arabidopsis: sequence characterization and basic exp						
	A;Reference number: 225337; MUID: 9972994						
	A;Accession: T51232						
	A;Status: preliminary; translated from GB/EMBL/DDBJ						
	A;Molecule type: mRNA						
	A;Residues: 1-808 <PYS>						
	A;Cross-references: EMBL:AF036309; PIDN: AAD24412.1						
	C;Genetics:						
	A;Gene: SC1L4						
Query Match 4 DHHHHQ-----DKTMMMFEDDGMDELLAVLGYKVRSEMDAQAQKLEQLEV 54							
	Best Local Similarity 16.4%; Score 453.5; DB 2; Length 808;						
	Matches 151; Conservative 91; Mismatches 185; Indels 159; Gaps 21;						
	Db	325 EHHHHSYAPPNRGKSHWRDDED-----EVEERSNKQSV-----	364	Db	301 RLTGIGPP--APDNFDYLHEVGCKLAHLAEAHVFEYRGVANTLADLASMULERLPE	358	
Qy	55 MMSVYQDDLSQLATEVHYNPAELYTWLDMSLTDLNPPSSNAEYDLKALPGD-AILNQ	112	Qy	301 RLTGIGPP--APDNFDYLHEVGCKLAHLAEAHVFEYRGVANTLADLASMULERLPE	358		
Db	365 --YVEESELSEM-----FNMEL-----	392	Db	327 EAYEYSSAVESLDMTLPRESQERNVERQCLARDVNIVACEGERTERYEAGKWRAR	296		
Qy	113 -FAIDASSSSQGGGGDTYTNKRLKCSNSGVEVTATASTRHVYLVQENGVRLVIA	171	Qy	415 ESLHYVSTLFDSSLE-GVP-SQCDKV-MSEVYLGKQICNVVACDGPDRVERHETLSQWRNR	471		
Db	393 NEPTESAKVYTAQSGAKINGKK-----STSTSHN----DSKKEPAPDLRPL	435	Db	472 FGSGAAFAAHIGS-----NAFKOSMALLAFNGGEYRVEESDGLMLGWHTRPLIAT	524		
Qy	172 LLACAAEYOKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARR-----IYRLS	224	Db	297 MMAGINPKPKMSAKVYINNIONLIQOYC-----NKYKUKEENGELHFCWEEKSILVIA	348		
Db	436 LVLCQAVSYDRTANEMMRQIRRHSSPQNGSERSLAIYFANSIAEARLAGTGTQIYTAL	495	Qy	525 SAWK 528			
Qy	225 PSQSPIDHSLSDTLDMH--FYETCPYLKEHFTANQAILEAFQGKVRVHIDFMSNSQGLQ	282	Db	349 SAWR 352			

